

SEQUENCE LISTING

<110> Ebner, Reinhard
Chopra, Arvind
Ruben, Steven M.

<120> Connective Tissue Growth Factor-3

<130> 1488.0630002

<150> US 60/030,720

<151> 1996-11-08

<150> US 08/966,020

<151> 1997-11-07

<160> 13

<170> PatentIn version 3.0

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ctc tgc ctc ctc tca aag gtg cgt acc cag ctg tgc ccg aca cca tgt      95
Leu Cys Leu Leu Ser Lys Val Arg Thr Gln Leu Cys Pro Thr Pro Cys
-5                -1 1                                5                10

acc tgc ccc tgg cca cct ccc cga tgc ccg ctg gga gta ccc ctg gtg      145
Thr Cys Pro Trp Pro Pro Pro Arg Cys Pro Leu Gly Val Pro Leu Val
                15                                20                25

ctg gat ggc tgt ggc tgc tgc cgg gta tgt gca cgg cgg ctg ggg gag      195
Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Arg Arg Leu Gly Glu
                30                                35                40

ccc tgc gac caa ctc cac gtc tgc gac gcc agc cag ggc ctg gtc tgc      245
Pro Cys Asp Gln Leu His Val Cys Asp Ala Ser Gln Gly Leu Val Cys
                45                                50                55

cag ccc ggg gca gga ccc ggt ggc cgg ggg gcc ctg tgc ctc ttg gca      295
Gln Pro Gly Ala Gly Pro Gly Gly Arg Gly Ala Leu Cys Leu Leu Ala
60                65                                70                75

gag gac gac agc agc tgt gag gtg aac ggc cgc ctg tat cgg gaa ggg      335
Glu Asp Asp Ser Ser Cys Glu Val Asn Gly Arg Leu Tyr Arg Glu Gly
                80                                85                90

gag acc ttc cag ccc cac tgc agc atc cgc tgc cgc tgc gag gac ggc      385
Glu Thr Phe Gln Pro His Cys Ser Ile Arg Cys Arg Cys Glu Asp Gly
                95                                100                105

ggc ttc acc tgc gtg ccg ctg tgc agc gag gat gtg cgg ctg ccc agc      435
Gly Phe Thr Cys Val Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser
                110                                115                120

tgg gac tgc ccc cac ccc agg agg gtc gag gtc ctg ggc aag tgc tgc      485
Trp Asp Cys Pro His Pro Arg Arg Val Glu Val Leu Gly Lys Cys Cys
                125                                130                135

cct gag tgg gtg tgc ggc caa gga ggg gga ctg ggg acc cag ccc ctt      535
Pro Glu Trp Val Cys Gly Gln Gly Gly Leu Gly Thr Gln Pro Leu
140                145                                150                155

cca gcc caa gga ccc cag ttt tct ggc ctt gtc tct tcc ctg ccc cct      575
Pro Ala Gln Gly Pro Gln Phe Ser Gly Leu Val Ser Ser Leu Pro Pro
                160                                165                170

ggg gtc ccc tgc cca gaa tgg agc acg gcc tgg gga ccc tgc tgc acc      625
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|---|-----|-----|------|
| Gly Val Pro Cys Pro Glu Trp Ser Thr Ala Trp Gly Pro Cys Ser Thr | | | |
| 175 | 180 | 185 | |
| acc tgt ggg ctg ggc atg gcc acc cgg gtg tcc aac cag aac cgc ttc | | | 674 |
| Thr Cys Gly Leu Gly Met Ala Thr Arg Val Ser Asn Gln Asn Arg Phe | | | |
| 190 | 195 | 200 | |
| tgc cga ctg gag acc cag cgc cgc ctg tgc ctg tcc agg ccc tgc cca | | | 722 |
| Cys Arg Leu Glu Thr Gln Arg Arg Leu Cys Leu Ser Arg Pro Cys Pro | | | |
| 205 | 210 | 215 | |
| ccc tcc agg ggt cgc agt cca caa aac agt gcc ttc tagagccggg | | | 768 |
| Pro Ser Arg Gly Arg Ser Pro Gln Asn Ser Ala Phe | | | |
| 220 | 225 | 230 | |
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| gctgatggaa gatgggtccgt gcccaggccc ttggctgcag gcaacacatt agcctgggtcc | | | 833 |
| caccatgcag aacaccaata ttaacacgct gcctgggtctg tctggatccc gaggtatggc | | | 943 |
| agaggtgcaa gacctagtcc cctttcctct aactcactgc ctaggaggct ggccaagggtg | | | 1003 |
| tccagggtcc tctagcccac tccctgccta cacacacagc ctatatcaaa catgcacacg | | | 1063 |
| ggcgagcttt ctctccgact tcccctgggc aagagatggg acaagcagtc ccttaatat | | | 1123 |
| gaggctgcag caggtgctgg gctggactgg ccatttttct gggggtagga tgaagagaag | | | 1183 |
| gcacacagag attctggatc tcctgctgcc ttttctggag ttgtaaaaat tgttccctgaa | | | 1243 |
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<213> Homo sapiens

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| | | | |
|---|---|----|--|
| Leu Leu Ser Lys Val Arg Thr Gln Leu Cys Pro Thr Pro Cys Thr Cys | | | |
| -1 1 | 5 | 10 | |

| | | | |
|---|----|----|--|
| Pro Trp Pro Pro Pro Arg Cys Pro Leu Gly Val Pro Leu Val Leu Asp | | | |
| 15 | 20 | 25 | |

| | | | |
|---|----|----|----|
| Gly Cys Gly Cys Cys Arg Val Cys Ala Arg Arg Leu Gly Glu Pro Cys | | | |
| 30 | 35 | 40 | 45 |

Asp Gln Leu His Val Cys Asp Ala Ser Gln Gly Leu Val Cys Gln Pro
50 55 60

Gly Ala Gly Pro Gly Gly Arg Gly Ala Leu Cys Leu Leu Ala Glu Asp
65 70 75

Asp Ser Ser Cys Glu Val Asn Gly Arg Leu Tyr Arg Glu Gly Glu Thr
80 85 90

Phe Gln Pro His Cys Ser Ile Arg Cys Arg Cys Glu Asp Gly Gly Phe
95 100 105

Thr Cys Val Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser Trp Asp
110 115 120 125

Cys Pro His Pro Arg Arg Val Glu Val Leu Gly Lys Cys Cys Pro Glu
130 135 140

Trp Val Cys Gly Gln Gly Gly Gly Leu Gly Thr Gln Pro Leu Pro Ala
145 150 155

Gln Gly Pro Gln Phe Ser Gly Leu Val Ser Ser Leu Pro Pro Gly Val
160 165 170

Pro Cys Pro Glu Trp Ser Thr Ala Trp Gly Pro Cys Ser Thr Thr Cys
175 180 185

Gly Leu Gly Met Ala Thr Arg Val Ser Asn Gln Asn Arg Phe Cys Arg
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Arg Gly Arg Ser Pro Gln Asn Ser Ala Phe
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<213> Homo sapiens

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Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
50 55 60

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
65 70 75 80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
85 90 95

Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
100 105 110

Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
115 120 125

Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
130 135 140

Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
145 150 155 160

Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
165 170 175

Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
180 185 190

Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
195 200 205

Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
210 215 220

Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
225 230 235 240

Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
245 250 255

Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
260 265 270

Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
275 280 285

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
290 295 300

Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
305 310 315 320

Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
325 330 335

Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
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36

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32

<210> 6

<211> 39

<212> DNA

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<400> 6

cggcaggatc cgccatcatg agaggcacac cgaagaccc

39

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32

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ggtctgtntg gatcccgagg tatggcagag gtgcaagacc tagtctctt tctctaaact 130
cactgcctag gaggctggcc aagggtgtcca gggctctcta gcccaacttc tgcctacaca 240
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cgctgggagt acccctggtg ctggatggct gtggctgctg ccgngttat gtgcacggcg 180
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gcccactccc tgcctacaca cacagcctat atcaaacatg cacacgggag agctttctct 180
ccgacttccc ctgggcaaga gatgggacaa gcagtcctt aatattgagg ctgcagcagg 240
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